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Ramsay, L., M. Macaulay, S. degli Ivanissevich, K. MacLean, L. Cardle, J. Fuller, K. J. Edwards, S. Tuvesson, M. Morgante, A. Massari, E. Maestri, N. Marmiroli, T. Sjakste, M. Ganal, W. Powell and R. Waugh, A simple sequence repeat-based linkage map of barley 1997–2005

Reynolds, Mary G., Compensatory evolution in rifampin-resistant *Escherichia coli* 1471–1481

Riera-Lizarazu, O., M. I. Vales, E. V. Ananiev, H. W. Rines and R. L. Phillips, Production and characterization of maize chromosome 9 radiation hybrids derived from an oat-maize addition line 327–339

Robatzek, Merrilee, and James H. Thomas, Calcium/calmodulin-dependent protein kinase II regulates *Caenorhabditis elegans* locomotion in concert with a G_o/G_q signaling network 1069–1082

Rothenfluh, Adrian, Marla Abodeely, Jeffrey L. Price and Michael W. Young, Isolation and analysis of six *timeless* alleles that cause short- or long-period circadian rhythms in Drosophila 665–675

Ruiz, M. Fernanda, M. Rosario Esteban, Carmen Doñoro, Clara Goday and Lucas Sánchez, Evolution of dosage compensation in Diptera: The gene *maleless* implements dosage compensation in Drosophila (Brachycera suborder) but its homolog in Sciara (Nematocera suborder) appears to play no role in dosage compensation 1853–1865

Rusch, Douglas B., and Thomas C. Kaufman, Regulation of *proboscipedia* in Drosophila by homeotic selector genes 183–194

Ruvinsky, Ilya, Lee M. Silver and Jeremy J. Gibson-Brown, Phylogenetic analysis of T-box genes demonstrates the importance of amphioxus for understanding evolution of the vertebrate genome 1249–1257

Schierup, Mikkel H., and Jotun Hein, Consequences of recombination on traditional phylogenetic analysis 879–891

Schneider, Dominique, Esther Duperchy, Evelyne Coursange, Richard E. Lenski and Michel Blot, Long-term experimental evolution in *Escherichia coli*. IX. Characterization of insertion sequence-mediated mutations and rearrangements 477–488

Serrano-Cartagena, José, Héctor Candela, Pedro Robles, María Rosa Ponce, José Manuel Pérez-Pérez, Pedro Piqueras and José Luis Micol, Genetic analysis of *incurvata* mutants reveals three independent genetic operations at work in Arabidopsis leaf morphogenesis 1363–1377

Shitara, Hiroshi, Hideki Kaneda, Akitsugu Sato, Kimiko Inoue, Atsuo Ogura, Hiromichi Yonekawa and Jun-Ichi Hayashi, Selective and continuous elimination of mitochondria microinjected into mouse eggs from spermatids, but not from liver cells, occurs throughout embryogenesis 1277–1284

Singer, Jason M., Greg J. Hermann and Janet M. Shaw, Suppressor of *mdm20* in yeast identify new alleles of *ACT1* and *TPM1* predicted to enhance actin-tropomyosin interactions 523–534

Sitcheran, Raquel, Roger Emter, Anastasia Kralli and Keith R. Yamamoto, A genetic analysis of glucocorticoid receptor signaling: Identification and characterization of ligand-effect modulators in *Saccharomyces cerevisiae* 963–972

Slatkin, Montgomery, and Christina A. Muirhead, A method for estimating the intensity of overdominant selection from the distribution of allele frequencies 2119–2126

Sorensen, D., A. Vernersen and S. Andersen, Bayesian analysis of response to selection: A case study using litter size in Danish Yorkshire pigs 283–295

Srivastava, Amit, Carol A. Woolford and Elizabeth W. Jones, Pep3p/Pep5p complex: A putative docking factor at multiple steps of vesicular transport to the vacuole of *Saccharomyces cerevisiae* 105–122

Stefanov, Valeri T., Distribution of genome shared identical by descent by two individuals in grandparent-type relationship 1403–1410

Takano-Shimizu, Toshiyuki, Genetic screens for factors involved in the notum bristle loss of interspecific hybrids between *Drosophila melanogaster* and *D. simulans* 269–282

Tanenbaum, Sara B., Sharon M. Gorski, Jamie C. Rusconi and Ross L. Cagan, A screen for dominant modifiers of the *irreC-rst* cell death phenotype in the developing Drosophila retina 205–217

Templeton, Alan R., Kenneth M. Weiss, Deborah A. Nickerson, Eric Boerwinkle and Charles F. Sing, Cladistic structure within the human *lipoprotein lipase* gene and its implications for phenotypic association studies 1259–1275

Teuscher, F., G. A. Brockmann, P. E. Rudolph, H. H. Swalve and V. Guiard, Models for chromatid interference with applications to recombination data 1449–1460

Therrien, Marc, Deborah K. Morrison, Allan M. Wong and Gerald M. Rubin, A genetic screen for modifiers of a kinase suppressor of Ras-dependent rough eye phenotype in Drosophila 1231–1242

Tirián, László, Jaakko Puro, Miklós Erdélyi, Imre Boros, Bernadett Papp, Mónika Lippai and János Szabad, The *Ketel*^{D} dominant-negative mutations identify maternal function of the Drosophila importin-β gene required for cleavage nuclei formation 1901–1912

Turner, Paul E., and Santiago F. Elena, Cost of host radiation in an RNA virus 1465–1470

Uyenoyama, Marcy K., Evolutionary dynamics of self-incompatibility alleles in Brassica 351–359

van der Gaag, Marijn, Alfons J. M. Debets, Jessica Oosterhof, Marijke Slakhorst, Jessica A. G. M. Thijssen and Rolf F. Hoekstra, Spore-killing meiotic drive factors in a natural population of the fungus *Podospora anserina* 593–605

Vaskova, Martina, A. M. Bentley, Samantha Marshall, Pamela Reid, Carl S. Thummel and Andrew J. Andres, Genetic analysis of the Drosophila 63F early puff: Characterization of mutations in *E63-1* and *maggie*, a putative Tom22 229–244

Verrelli, Brian C., and Walter F. Eanes, Extensive amino acid polymorphism at the *Pgm* locus is consistent with adaptive protein evolution in *Drosophila melanogaster* 1737–1752

Vinella, Daniel, Michael Cashel and Richard D'Ari, Selected amplification of the cell division genes *ftsQ-ftsA-ftsZ* in *Escherichia coli* 1483–1492

Vrána, Jan, Marie Kubaláková, Hana Šimková, Jarmila Číhalíková, Martin A. Lysák and Jaroslav Doležel, Flow sorting of mitotic chromosomes in common wheat (*Triticum aestivum* L.) 2033–2041

Wahl, Lindi M., and David C. Krakauer, Models of experimental evolution: The role of genetic chance and selective necessity 1437–1448

Weinreich, Daniel M., and David M. Rand, Contrasting patterns of nonneutral evolution in proteins encoded in nuclear and mitochondrial genomes 385–399

Welcker, Anne J., Jacky de Montigny, Serge Potier and Jean-Luc Souciet, Involvement of very short DNA tandem repeats and the influence of the *RAD52* gene on the occurrence of deletions in *Saccharomyces cerevisiae* 549–557

Welton, Robert M., and Charles S. Hoffman, Glucose monitoring in fission yeast via the gpa2 Gα, the git5 Gβ and the git3 putative glucose receptor 513–521

Wen, Yu, Duc Nguyen, Ying Li and Zhi-Chun Lai, The N-terminal BTB/POZ domain and C-terminal sequences are essential for Tramtrack69 to specify cell fate in the developing Drosophila eye 195–203

Windsor, Aaron J., and Candace S. Waddell, *FARE*, a new family of foldback transposons in Arabidopsis 1983–1995

Winge, Per, Tore Brembu, Ralf Kristensen and Atle M. Bones, Genetic structure and evolution of RAC-GTPases in *Arabidopsis thaliana* 1959–1971

Xiao, Yong-Li, Xianggan Li and Thomas Peterson, *Ac* insertion site affects the frequency of transposon-induced homologous recombination at the maize *p1* locus 2007–2017

Yamamoto, Rochele R., J. Myles Axton, Yutaka Yamamoto, Robert D. C. Saunders, David M. Glover and Daryl S. Henderson, The Drosophila *mus101* gene, which links DNA repair, replication and condensation of heterochromatin in mitosis, encodes a protein with seven BRCA1 C-terminus domains 711–721

Yi, Nengjun, and Shizhong Xu, Bayesian mapping of quantitative trait loci under the identity-by-descent-based variance component model 411–422

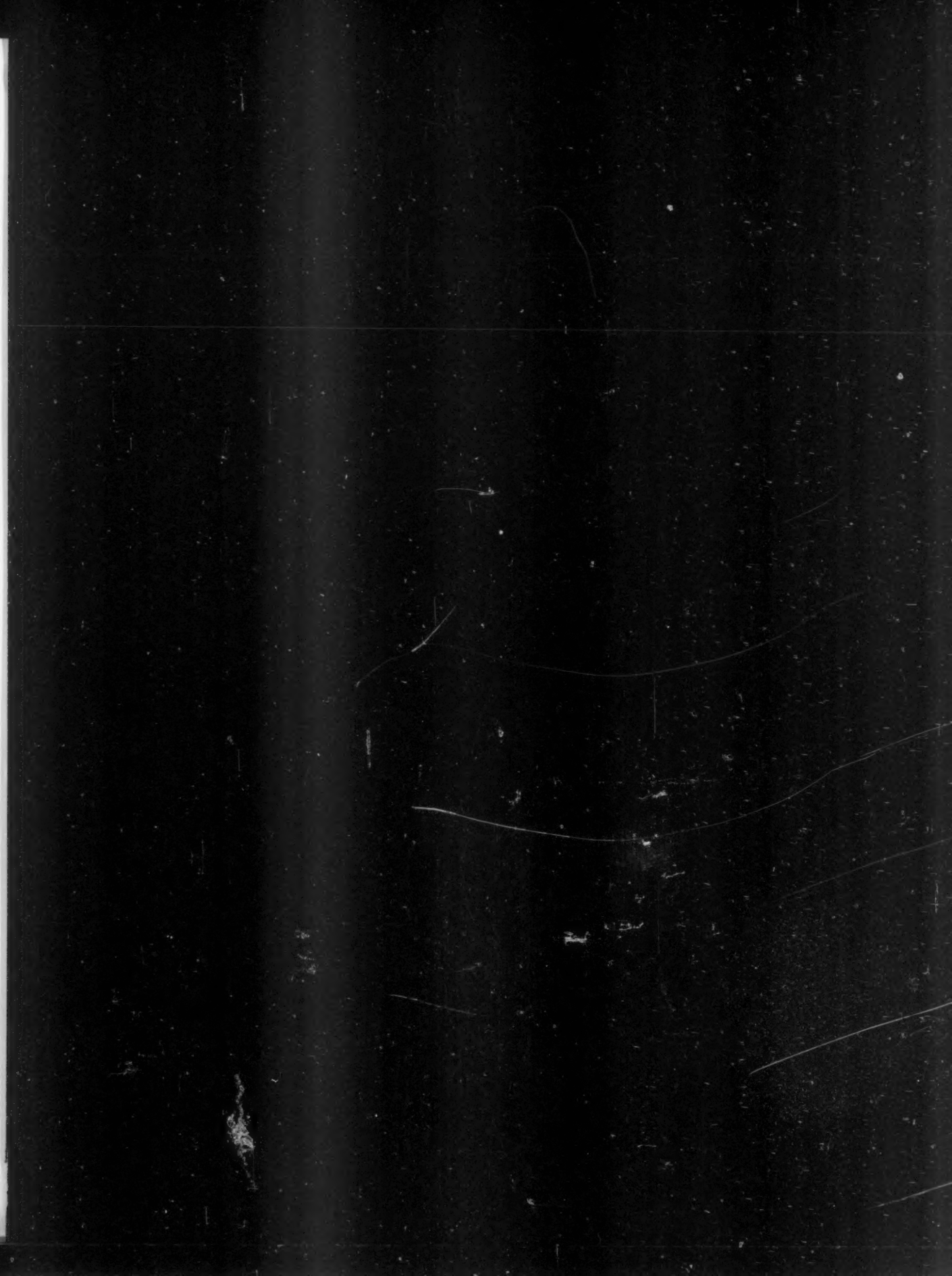
Yi, Soojin, and Brian Charlesworth, A selective sweep associated with a recent gene transposition in *Drosophila miranda* 1753–1763

Yu, Hung-Hsiang, Alex S. Huang and Alex L. Kolodkin, Semaphorin-1a acts in concert with the cell adhesion molecules fasciclin II and connectin to regulate axon fasciculation in Drosophila 723–731

Yu, Zhihui, Stephen I. Wright and Thomas E. Bureau, *Mutator*-like elements in *Arabidopsis thaliana*: Structure, diversity and evolution 2019–2031

Yuan, Daniel S., Zinc-regulated genes in *Saccharomyces cerevisiae* revealed by transposon tagging 45–58

Yun, Bokyoung, Kun Lee, Robert Farkaš, Christophe Hitte and Leonard Rabinow, The LAMMER protein kinase encoded by the *Doa* locus of Drosophila is required in both somatic and germline cells and is expressed as both nuclear and cytoplasmic isoforms throughout development 749–761

Zhang, Jianzhi, and Helene F. Rosenberg, Sequence variation at two eosinophil-associated ribonuclease loci in humans 1949–1958

Zolman, Bethany K., Andrea Yoder and Bonnie Bartel, Genetic analysis of indole-3-butyric acid responses in *Arabidopsis thaliana* reveals four mutant classes 1323–1337